

(1) GENERAL INFORMATION:

- AATGAAGAAC TGCTTAGTTT

20

- AATCAAGGAA TTTAACTG

18

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1788 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 156..1683
 (D) OTHER INFORMATION: /function= "Nucleotides 156 through
 1683 encode the amino acid sequence for
 the Hamster Scavenger Receptor Class
 B-I."
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCACCTGCA GGGCTACTGC TGCTCCGGCC ACTGCCTGAG ACTCACCTTG CTGGAACGTG 60
AGCCTCGGCT TCTGTCATCT CTGTGGCCTC TGTCGCTTCT GTCGCTGTCC CCCTTCAGTC 120
CCTGAGCCCC GCGAGCCCGG GCCGCACACG CGGACATGGG CGGCAGCGCC AGGGCGCGCT 180
GGGTGGCGGT GGGGCTGGGC GTCGTGGGGC TGCTGTGCGC TGTGCTCGGT GTGGTTATGA 240
TCCTCGTGAT GCCCTCGCTC ATCAAACAGC AGGTACTGAA GAATGTCCGC ATAGACCCCA 300
GCAGCCTGTC CTTTGCAATG TGGAAGGAGA TCCCTGTACC CTTCTACTTG TCCGTCTACT 360
TCTTCGAGGT GGTCAATCCC AGCGAGATCC TAAAGGGTGA GAAGCCAGTA GTGCGGGAGC 420
GTGGACCCTA TGTCTACAGG GAATTCAGAC ATAAGGCCAA CATCACCTTC AATGACAATG 480
ATACTGTGTC CTTTGTGGAG CACCGCAGCC TCCATTTCCA GCCGGACAGG TCCCACGGCT 540
CTGAGAGTGA CTACATTATA CTGCCTAACA TTCTGGTCTT GGGGGGCGCA GTAATGATGG 600
AGAGCAAGTC TGCAGGCCTG AAGCTGATGA TGACCTTGGG GCTGGCCACC TTGGGCCAGC 660
GTGCCTTTAT GAACCGAACA GTTGGTGAGA TCCTGTGGGG CTATGAGGAT CCCTTCGTGA 720
ATTTTATCAA CAAATACTTA CCAGACATGT TCCCCATCAA GGGCAAGTTC GGCCTGTTTG 780
TTGAGATGAA CAACTCAGAC TCTGGGCTCT TCACTGTGTT CACGGGCGTC CAGAACTTCA 840
GCAAGATCCA CCTGGTGGAC AGATGGAATG GGCTCAGCAA GGTCAACTAC TGGCATTGAG 900
AGCAGTGCAA CATGATCAAT GGCACCTCCG GGCAGATGTG GGCACCATTC ATGACACCCC 960
AGTCCTCGCT GGAATTCTTC AGTCCGGAAG CCTGCAGGTC TATGAAGCTC ACCTACCATG 1020
ATTCAGGGGT GTTTGAAGGC ATCCCCACCT ATCGCTTCAC AGCCCCTAAA ACTTTGTTTG 1080
CCAATGGGTC TGTTTACCCA CCAATGAAG GTTTCTGCCC GTGCCTTGAA TCCGGCATTC 1140
AAAATGTCAG CACTTGCAGG TTTGGTGCAC CCCTGTTTCT GTCACACCCT CACTTCTACA 1200
ATGCAGACCC TGTGCTATCA GAAGCCGTTT TGGGTCTGAA CCCTGACCCA AGGGAGCATT 1260
CTTTGTTTCT TGACATCCAT CCGGTCACTG GGATCCCCAT GAACTGTTCT GTGAAGTTGC 1320
AGATAAGCCT CTACATCAAA GCTGTCAAGG GCATTGGGCA AACAGGGAAG ATCGAGCCCCG 1380
TGGTCTCCC ATTGCTGTGG TTTGAGCAGA GCGGTGCCAT GGGCGGCGAG CCCCTGAACA 1440
CGTTCTACAC GCAGCTGGTG CTGATGCCCC AGGTACTTCA GTATGTGCAG TATGTGCTGC 1500
TGGGGCTGGG CGGCCTCCTG CTGCTGGTGC CCGTCATCTA CCAGTTGCGC AGCCAGGAGA 1560

"B-I" RECEPTOR

AATGCTTTTT ATTTTGGAGT GGTAGTAAAA AGGGCTCGCA GGATAAGGAG GCCATTCAGG 1620
 CCTACTCTGA GTCTCTGATG TCACCAGCTG CCAAGGGCAC GGTGCTGCAA GAAGCCAAGC 1680
 TGTAGGGTCC CAAAGACACC ACGAGCCCCC CCAACCTGAT AGCTTGGTCA GACCAGCCAT 1740
 CCAGCCCCTA CACCCCGCTT CTTGAGGACT CTCTCAGCGG ACAGTCGC 1788

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..509

(D) OTHER INFORMATION: /function= "Amino acid sequence for the Hamster Scavenger Receptor Class B-I."

(ix) FEATURE:

- (A) NAME/KEY: Domain
- (B) LOCATION: 9..32

(D) OTHER INFORMATION: /note= "Putative transmembrane domain."

(ix) FEATURE:

- (A) NAME/KEY: Domain
- (B) LOCATION: 440..464

(D) OTHER INFORMATION: /note= "Putative transmembrane domain."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..385

(D) OTHER INFORMATION: /note= "Positions 102-104, 108-110, 173-175, 212-214, 227-229, 255-257, 310-312, 330-332 and 383-385 represent potential N-linked glycosylation sites."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21..470

(D) OTHER INFORMATION: /note= "The cysteines at positions 21, 251, 280, 321, 323, 334, 384 and 470 represent potential disulfide linkages."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Gly Ser Ala Arg Ala Arg Trp Val Ala Val Gly Leu Gly Val
 1 5 10 15

Val Gly Leu Leu Cys Ala Val Leu Gly Val Val Met Ile Leu Val Met
 20 25 30

Pro Ser Leu Ile Lys Gln Gln Val Leu Lys Asn Val Arg Ile Asp Pro
 35 40 45

Ser Ser Leu Ser Phe Ala Met Trp Lys Glu Ile Pro Val Pro Phe Tyr
 50 55 60

Leu Ser Val Tyr Phe Phe Glu Val Val Asn Pro Ser Glu Ile Leu Lys
 65 70 75 80

Gly Glu Lys Pro Val Val Arg Glu Arg Gly Pro Tyr Val Tyr Arg Glu
 85 90 95

Phe Arg His Lys Ala Asn Ile Thr Phe Asn Asp Asn Asp Thr Val Ser
 100 105 110

Phe Val Glu His Arg Ser Leu His Phe Gln Pro Asp Arg Ser His Gly
 115 120 125

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 262200 00150400

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Ser Glu Ser Asp Tyr Ile Ile Leu Pro Asn Ile Leu Val Leu Gly Gly
 130 135 140
 Ala Val Met Met Glu Ser Lys Ser Ala Gly Leu Lys Leu Met Met Thr
 145 150 155 160
 Leu Gly Leu Ala Thr Leu Gly Gln Arg Ala Phe Met Asn Arg Thr Val
 165 170 175
 Gly Glu Ile Leu Trp Gly Tyr Glu Asp Pro Phe Val Asn Phe Ile Asn
 180 185 190
 Lys Tyr Leu Pro Asp Met Phe Pro Ile Lys Gly Lys Phe Gly Leu Phe
 195 200 205
 Val Glu Met Asn Asn Ser Asp Ser Gly Leu Phe Thr Val Phe Thr Gly
 210 215 220
 Val Gln Asn Phe Ser Lys Ile His Leu Val Asp Arg Trp Asn Gly Leu
 225 230 235 240
 Ser Lys Val Asn Tyr Trp His Ser Glu Gln Cys Asn Met Ile Asn Gly
 245 250 255
 Thr Ser Gly Gln Met Trp Ala Pro Phe Met Thr Pro Gln Ser Ser Leu
 260 265 270
 Glu Phe Phe Ser Pro Glu Ala Cys Arg Ser Met Lys Leu Thr Tyr His
 275 280 285
 Asp Ser Gly Val Phe Glu Gly Ile Pro Thr Tyr Arg Phe Thr Ala Pro
 290 295 300
 Lys Thr Leu Phe Ala Asn Gly Ser Val Tyr Pro Pro Asn Glu Gly Phe
 305 310 315 320
 Cys Pro Cys Leu Glu Ser Gly Ile Gln Asn Val Ser Thr Cys Arg Phe
 325 330 335
 Gly Ala Pro Leu Phe Leu Ser His Pro His Phe Tyr Asn Ala Asp Pro
 340 345 350
 Val Leu Ser Glu Ala Val Leu Gly Leu Asn Pro Asp Pro Arg Glu His
 355 360 365
 Ser Leu Phe Leu Asp Ile His Pro Val Thr Gly Ile Pro Met Asn Cys
 370 375 380
 Ser Val Lys Leu Gln Ile Ser Leu Tyr Ile Lys Ala Val Lys Gly Ile
 385 390 395 400
 Gly Gln Thr Gly Lys Ile Glu Pro Val Val Leu Pro Leu Leu Trp Phe
 405 410 415
 Glu Gln Ser Gly Ala Met Gly Gly Glu Pro Leu Asn Thr Phe Tyr Thr
 420 425 430
 Gln Leu Val Leu Met Pro Gln Val Leu Gln Tyr Val Gln Tyr Val Leu
 435 440 445
 Leu Gly Leu Gly Gly Leu Leu Leu Leu Val Pro Val Ile Tyr Gln Leu
 450 455 460
 Arg Ser Gln Glu Lys Cys Phe Leu Phe Trp Ser Gly Ser Lys Lys Gly
 465 470 475 480
 Ser Gln Asp Lys Glu Ala Ile Gln Ala Tyr Ser Glu Ser Leu Met Ser
 485 490 495
 Pro Ala Ala Lys Gly Thr Val Leu Gln Glu Ala Lys Leu

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500

505

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2032 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc. feature
- (B) LOCATION: 40..1926

- (D) OTHER INFORMATION: /Function = "Nucleotides 40 through 1926 encode the amino acid sequence for the Drosophila Melanogaster Scavenger Receptor Class CI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GACCGTATCT ATACATTAAG TTCGTAATAT CTCTGCGGAA TGAATTTTT CTGGACTCTG      60
GCTGTGATTG TGATATATTG TATAGGTCAC ATTCATGGAC GATGTGAAAG ATCTATAGAT      120
TTGGATAATG GAAGTATAAA TTATCGACAG AGAAATATAG TGAGATTCAG ATGCAATCGC      180
GGCTACACTT TGCAGGGAAC AGTAATGCAA ACTTGCGATC GAGATGGTCG CCTTCGAGGC      240
GAAAAACCAT TCTGTGCCAG TAGGGGATGT GCGAGGCCCG AGGATCCGGA GAACGGACAC      300
GTCGAAAATC TTTCCCTAAG GCGGATGTC GTGTGCCACG ATGGCTATGT CTTGGTCGGT      360
GGTCGCACTG CCTACTGCGA TGGAGAAAGA TGGAGCACCC AGCTGGGATC GTGTCGAAGG      420
AGCAACCACA CAAGAGATCA TTCTTGCGAT TTCGAGAGCG AGGATCAGTG CGGTTGGGAG      480
GCGGAGACAA CCTTCCGACG ACCCTGGAAG CGAGTCAGCA CGGTATCCGA TATTCCTCC      540
CTAAGAACGG GACCCCGCCA CGATCACACG TTTAAAAACG AATCCGGTGG TCATTACATG      600
CGCATGGAAA CCCAAATGGG GGCTTATGGA AGCTACCATC TGCTATCGCC GATCTATCCC      660
AGATCCCTCA CCCTGAAGAC CGCCTGCTGC TTTCGATTCC ACTACTTCAT GTTTGGCGCT      720
GGTGTGGATA ATCTGGTGGT GTCCGTTAAA CCCGTTTCGA TGCCAATGGC AACCATGTGG      780
AATAGGTTCA GAGCCAATTG CAGCAAATTT GAGATATCTG GTCAGCAGGG AACCCAGTGG      840
CTAGAGCACA CGATCAGCAT TGACGAGATG CAAGAGGACT TCCAGGTGAT ATTCACGGCA      900
ACGGATGCAA GATCCCAATT CGGAGATATT GCCATCGATG ATGTAAAGCT AATGACAGGC      960
AGTGAGTGTG GCACAAACGG ATTTAGCACC ACCACAGAAC CAACGGCTCC GACAGGCAGC     1020
AACGAGCAAC CACTGGTCTA CGATATGATA AGTTGTTTCA GTCGATGCGG AACATCAATG     1080
TCGGCCTCCA ATATAACCAA CAATGGTATA GTCATGGGAT GTGGATGTAA TGACGAGTGC     1140
CTTTCGGATG AGACTTGTTG CCTAAACTAT TTGGAGGAGT GCACAAAGGA GCTGCTCACC     1200
ACGACCGAGG ATGATATTAG TTCCCTGCCC CCAACGGTCA CATCAACAAG CACAAGCACT     1260
ACGAGGAAGT CAACAACAAC AACAACCACA AGCAGGACTA CTACAAGTAC AACAACAACCT     1320
AAAAGGCCAA CCACAACCAC AACAACAACA AAGGCCACAA CTACAAAGCG AACAACAACC     1380
ACTAAAAAAC CGACAACAAC TTCAACAACG CCGAAGCCAA CAACAACGAC TTCAACCACA     1440
CCAAAGTCTA CAACTTCTAC AACGTCTACA ACTTCAACAA CACCAACGAC AACAACCTACA     1500

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ATAAATGTGT TTACAACAAA GAAAACAACA ATAATGATCC CTACTTCCAG TACCGAAAAG 1560
 ACTACAGGCA TCATCACCAC CATGAAGACA CGCAAGCGCA TCACTTGGA CGTTGATCCT 1620
 CAGGACATCG AGGGTCACAT GGACACGAGC GGAAGTACCC CCAATCCAGC TTTAGTAGTA 1680
 CTTTACCTGC TACTCGGCAT TGTTCTGGTG GTAGTTCTGG CCAACGTCGT TAATCGCTGG 1740
 ATAATACCAA TCACTGGATC AAAGACCAGC AGCGAAAAGG CTGTGAGATT CAAGAAGGCA 1800
 TTCGATAGTC TGAAGAAGCA ACGGAAAAGA AACAGCATGG ATGATCAGCC GTTATGCGAC 1860
 TCCGATAACG ACGATGTAGA GTATTTTCGAA GAAATGGGCG TGGACATACG ACATAGGACC 1920
 GATCTATGAG GGTAATCCCC AGTGATACCA AAACAAACGC TTAGGCCTGT GCCTATTGTA 1980
 TAGGATGTTT CTAAATGTGT ATGCAAGAAT CGAATAAAAG AAAATATGCA AC 2032

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 629 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
 - (A) NAME/KEY: misc. feature
 - (B) LOCATION: 1..629
 - (D) OTHER INFORMATION: /Function = "Amino acid sequence for the Drosophila Melanogaster Scavenger Receptor Class CI."
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 30..353
 - (D) OTHER INFORMATION: /note= "Positions 30-32, 90-92, 129-131, 180-182, 253-255 and 351-353 represent potential N-glycosylation sites."
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..20
 - (D) OTHER INFORMATION: /note= "Amino acids 1-20 represent a putative signal sequence."
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 21..74
 - (D) OTHER INFORMATION: /note= "Amino acids 21-74 represent complement control protein domain number 1."
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 75..127
 - (D) OTHER INFORMATION: /note= "Amino acids 75-127 represent complement control protein domain number 2."
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 128..312
 - (D) OTHER INFORMATION: /note= "Amino acids 128-312 represent an MAM domain."
- (ix) FEATURE:
 - (A) NAME/KEY: Disulfide-bond
 - (B) LOCATION: 22..381
 - (D) OTHER INFORMATION: /note= "The cysteines at positions 22, 45, 59, 72, 77, 99, 113, 125, 136, 144, 216, 217, 254, 310, 339, 343, 361, 363, 367, 373, 374 and 381 represent potential disulfide linkages."
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site

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(B) LOCATION: 338..381
 (D) OTHER INFORMATION: /note= "Amino acids 338-381
 represent a somatomedin B domain."
 (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 387..514
 (D) OTHER INFORMATION: /note= "Amino acids 387-514
 represent a mucin-like potential
 O-linked glycosylation region."
 (ix) FEATURE:
 (A) NAME/KEY: Domain
 (B) LOCATION: 544..564
 (D) OTHER INFORMATION: /note= "Amino acids 544-565
 represent a putative TM domain."
 (ix) FEATURE:
 (A) NAME/KEY: Domain
 (B) LOCATION: 565..629
 (D) OTHER INFORMATION: /note= "Amino acids 565-629
 represent a putative cytoplasmic
 domain."
 (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 576..602
 (D) OTHER INFORMATION: /note= "Amino acids 576-579 and
 599-602 represent casein kinase II
 sites."
 (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 578..592
 (D) OTHER INFORMATION: /note= "Amino acids 578-580 and
 590-592 represent protein kinase C
 sites."
 (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 596..599
 (D) OTHER INFORMATION: /note= "Amino acids 596-599
 represent a cAMP protein kinase site."
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Phe	Phe	Trp	Thr	Leu	Ala	Val	Ile	Val	Ile	Tyr	Cys	Ile	Gly	1	5	10	15
His	Ile	His	Gly	Arg	Cys	Glu	Arg	Ser	Ile	Asp	Leu	Asp	Asn	Gly	Ser	20	25	30	
Ile	Asn	Tyr	Arg	Gln	Arg	Asn	Ile	Val	Arg	Phe	Arg	Cys	Asn	Arg	Gly	35	40	45	
Tyr	Thr	Leu	Gln	Gly	Thr	Val	Met	Gln	Thr	Cys	Asp	Arg	Asp	Gly	Arg	50	55	60	
Leu	Arg	Gly	Glu	Lys	Pro	Phe	Cys	Ala	Ser	Arg	Gly	Cys	Ala	Arg	Pro	65	70	75	80
Glu	Asp	Pro	Glu	Asn	Gly	His	Val	Glu	Asn	Leu	Ser	Leu	Arg	Ala	Asp	85	90	95	
Val	Val	Cys	His	Asp	Gly	Tyr	Val	Leu	Val	Gly	Gly	Arg	Thr	Ala	Tyr	100	105	110	
Cys	Asp	Gly	Glu	Arg	Trp	Ser	Thr	Gln	Leu	Gly	Ser	Cys	Arg	Arg	Ser	115	120	125	
Asn	His	Thr	Arg	Asp	His	Ser	Cys	Asp	Phe	Glu	Ser	Glu	Asp	Gln	Cys	130	135	140	
Gly	Trp	Glu	Ala	Glu	Thr	Thr	Phe	Arg	Arg	Pro	Trp	Lys	Arg	Val	Ser	145	150	155	160
Thr	Val	Ser	Asp	Ile	His	Ser	Leu	Arg	Thr	Gly	Pro	Arg	His	Asp	His				

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165										170					175				
Thr	Phe	Lys	Asn	Glu	Ser	Gly	Gly	His	Tyr	Met	Arg	Met	Glu	Thr	Gln				
			180					185					190						
Met	Gly	Ala	Tyr	Gly	Ser	Tyr	His	Leu	Leu	Ser	Pro	Ile	Tyr	Pro	Arg				
		195					200					205							
Ser	Leu	Thr	Leu	Lys	Thr	Ala	Cys	Cys	Phe	Arg	Phe	His	Tyr	Phe	Met				
	210					215					220								
Phe	Gly	Ala	Gly	Val	Asp	Asn	Leu	Val	Val	Ser	Val	Lys	Pro	Val	Ser				
225					230					235					240				
Met	Pro	Met	Ala	Thr	Met	Trp	Asn	Arg	Phe	Arg	Ala	Asn	Cys	Ser	Lys				
				245					250					255					
Phe	Glu	Ile	Ser	Gly	Gln	Gln	Gly	Thr	Gln	Trp	Leu	Glu	His	Thr	Ile				
			260					265					270						
Ser	Ile	Asp	Glu	Met	Gln	Glu	Asp	Phe	Gln	Val	Ile	Phe	Thr	Ala	Thr				
		275					280					285							
Asp	Ala	Arg	Ser	Gln	Phe	Gly	Asp	Ile	Ala	Ile	Asp	Asp	Val	Lys	Leu				
	290					295					300								
Met	Thr	Gly	Ser	Glu	Cys	Gly	Thr	Asn	Gly	Phe	Ser	Thr	Thr	Thr	Glu				
305					310					315					320				
Pro	Thr	Ala	Pro	Thr	Gly	Ser	Asn	Glu	Gln	Pro	Leu	Val	Tyr	Asp	Met				
				325					330					335					
Ile	Ser	Cys	Ser	Gly	Arg	Cys	Gly	Thr	Ser	Met	Ser	Ala	Ser	Asn	Ile				
			340					345					350						
Thr	Asn	Asn	Gly	Ile	Val	Met	Gly	Cys	Gly	Cys	Asn	Asp	Glu	Cys	Leu				
		355					360					365							
Ser	Asp	Glu	Thr	Cys	Cys	Leu	Asn	Tyr	Leu	Glu	Glu	Cys	Thr	Lys	Glu				
	370					375					380								
Leu	Leu	Thr	Thr	Thr	Glu	Asp	Asp	Ile	Ser	Ser	Leu	Pro	Pro	Thr	Val				
385					390					395					400				
Thr	Ser	Thr	Ser	Thr	Ser	Thr	Thr	Arg	Lys	Ser	Thr	Thr	Thr	Thr	Thr				
				405					410					415					
Thr	Ser	Thr	Thr	Thr	Thr	Ser	Thr	Thr	Thr	Thr	Lys	Arg	Pro	Thr	Thr				
			420					425					430						
Thr	Thr	Thr	Thr	Thr	Lys	Ala	Thr	Thr	Thr	Lys	Arg	Thr	Thr	Thr	Thr				
			435				440					445							
Lys	Lys	Pro	Thr	Thr	Thr	Ser	Thr	Thr	Pro	Lys	Pro	Thr	Thr	Thr	Thr				
	450					455					460								
Ser	Thr	Thr	Pro	Lys	Ser	Thr	Thr	Ser	Thr	Thr	Ser	Thr	Thr	Ser	Thr				
465					470					475					480				
Thr	Pro	Thr	Thr	Thr	Thr	Thr	Ile	Asn	Val	Phe	Thr	Thr	Lys	Lys	Thr				
				485					490					495					
Thr	Ile	Met	Ile	Pro	Thr	Ser	Ser	Thr	Glu	Lys	Thr	Thr	Gly	Ile	Ile				
			500					505					510						
Thr	Thr	Met	Lys	Thr	Arg	Lys	Arg	Ile	Thr	Trp	Asn	Val	Asp	Pro	Gln				
		515					520					525							

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Asp Ile Glu Gly His Met Asp Thr Ser Gly Ser Thr Pro Asn Pro Ala
 530 535 540

Leu Val Val Leu Tyr Leu Leu Gly Ile Val Leu Val Val Val Leu
 545 550 555 560

Ala Asn Val Val Asn Arg Trp Ile Ile Pro Ile Thr Gly Ser Lys Thr
 565 570 575

Ser Ser Glu Lys Ala Val Arg Phe Lys Lys Ala Phe Asp Ser Leu Lys
 580 585 590

Lys Gln Arg Lys Arg Asn Ser Met Asp Asp Gln Pro Leu Cys Asp Ser
 595 600 605

Asp Asn Asp Asp Val Glu Tyr Phe Glu Glu Met Gly Val Asp Ile Arg
 610 615 620

His Arg Thr Asp Leu
 625

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1785 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 51..1577

(D) OTHER INFORMATION: /Function = "Nucleotides 51 through
 1577 encode the amino acid sequence
 for the murine Scavenger Receptor
 Class BI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCGTCTCCTT CAGGTCCTGA GCCCCGAGAG CCCCTTCCGC GCACGCGGAC ATG GGC	56
Met Gly	
1	
GGC AGC TCC AGG GCG CGC TGG GTG GCC TTG GGG TTG GGC GCC CTG GGG	104
Gly Ser Ser Arg Ala Arg Trp Val Ala Leu Gly Leu Gly Ala Leu Gly	
5 10 15	
CTG CTG TTT GCT GCG CTC GGC GTT GTC ATG ATC CTC ATG GTG CCC TCC	152
Leu Leu Phe Ala Ala Leu Gly Val Val Met Ile Leu Met Val Pro Ser	
20 25 30	
CTC ATC AAG CAG CAG GTG CTC AAG AAT GTC CGC ATA GAC CCG AGC AGC	200
Leu Ile Lys Gln Gln Val Leu Lys Asn Val Arg Ile Asp Pro Ser Ser	
35 40 45 50	
CTG TCC TTC GGG ATG TGG AAG GAG ATC CCC GTC CCT TTC TAC TTG TCT	248
Leu Ser Phe Gly Met Trp Lys Glu Ile Pro Val Pro Phe Tyr Leu Ser	
55 60 65	
GTC TAC TTC TTC GAA GTG GTC AAC CCA AAC GAG GTC CTC AAC GGC CAG	296
Val Tyr Phe Phe Glu Val Val Asn Pro Asn Glu Val Leu Asn Gly Gln	
70 75 80	
AAG CCA GTA GTC CGG GAG CGT GGA CCC TAT GTC TAC AGG GAG TTC AGA	344
Lys Pro Val Val Arg Glu Arg Gly Pro Tyr Val Tyr Arg Glu Phe Arg	
85 90 95	
CAA AAG GTC AAC ATC ACC TTC AAT GAC AAC GAC ACC GTG TCC TTC GTG	392
Gln Lys Val Asn Ile Thr Phe Asn Asp Asn Asp Thr Val Ser Phe Val	
100 105 110	

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GAG Glu 115	AAC Asn	CGC Arg	AGC Ser	CTC Leu	CAT His 120	TTC Phe	CAG Gln	CCT Pro	GAC Asp 125	AAG Lys	TCG Ser	CAT His	GGC Gly	TCA Ser 130	GAG Glu 130	440
AGT Ser	GAC Asp	TAC Tyr	ATT Ile	GTA Val 135	CTG Leu	CCT Pro	AAC Asn	ATC Ile	TTG Leu 140	GTC Val	CTG Leu	GGG Gly	GGC Gly	TCG Ser 145	ATA Ile 145	488
TTG Leu	ATG Met	GAG Glu	AGC Ser 150	AAG Lys	CCT Pro	GTG Val	AGC Ser	CTG Leu 155	AAG Lys	CTG Leu	ATG Met	ATG Met	ACC Thr 160	TTG Leu 160	GCG Ala 160	536
CTG Leu	GTC Val	ACC Thr 165	ATG Met	GGC Gly	CAG Gln	CGT Arg	GCT Ala 170	TTT Phe	ATG Met	AAC Asn	CGC Arg	ACA Thr 175	GTT Val 175	GGT Gly	GAG Glu 175	584
ATC Ile 180	CTG Leu	TGG Trp	GGC Gly	TAT Tyr	GAC Asp	GAT Asp 185	CCC Pro	TTC Phe	GTG Val	CAT His	TTT Phe 190	CTC Leu	AAC Asn	ACG Thr	TAC Tyr 190	632
CTC Leu 195	CCA Pro	GAC Asp	ATG Met	CTT Leu	CCC Pro 200	ATA Ile	AAG Lys	GGC Gly	AAA Lys 205	TTT Phe	GGC Gly	CTG Leu	TTT Phe	GTT Val 210	GGG Gly 210	680
ATG Met	AAC Asn	AAC Asn	TCG Ser 215	AAT Asn	TCT Ser	GGG Gly	GTC Val	TTC Phe	ACT Thr 220	GTC Val	TTC Phe	ACG Thr	GGC Gly	GTC Val 225	CAG Gln 225	728
AAT Asn	TTC Phe	AGC Ser 230	AGG Arg	ATC Ile	CAT His	CTG Leu	GTG Val	GAC Asp 235	AAA Lys	TGG Trp	AAC Asn	GGA Gly	CTC Leu 240	AGC Ser 240	AAG Lys 240	776
ATC Ile	GAT Asp	TAT Tyr 245	TGG Trp	CAT His	TCA Ser	GAG Glu	CAG Gln 250	TGT Cys	AAC Asn	ATG Met	ATC Ile	AAT Asn 255	GGG Gly	ACT Thr	TCC Ser 255	824
GGG Gly 260	CAG Gln	ATG Met	TGG Trp	GCA Ala	CCC Pro	TTC Phe 265	ATG Met	ACA Thr	CCC Pro	GAA Glu	TCC Ser 270	TCG Ser	CTG Leu	GAA Glu	TTC Phe 270	872
TTC Phe 275	AGC Ser	CCG Pro	GAG Glu	GCA Ala	TGC Cys 280	AGG Arg	TCC Ser	ATG Met	AAG Lys 285	CTG Leu	ACC Thr	TAC Tyr	AAC Asn	GAA Glu 290	TCA Ser 290	920
AGG Arg	GTG Val	TTT Phe	GAA Glu	GGC Gly 295	ATT Ile	CCC Pro	ACG Thr	TAT Tyr	CGC Arg 300	TTC Phe	ACG Thr	GCC Ala	CCC Pro	GAT Asp 305	ACT Thr 305	968
CTG Leu	TTT Phe	GCC Ala	AAC Asn 310	GGG Gly	TCC Ser	GTC Val	TAC Tyr	CCA Pro 315	CCC Pro	AAC Asn	GAA Glu	GGC Gly	TTC Phe 320	TGC Cys 320	CCA Pro 320	1016
TGC Cys	CGA Arg	GAG Glu 325	TCT Ser	GGC Gly	ATT Ile	CAG Gln	AAT Asn 330	GTC Val	AGC Ser	ACC Thr	TGC Cys	AGG Arg 335	TTT Phe	GGT Gly	GCG Ala 335	1064
CCT Pro 340	CTG Leu	TTT Phe	CTC Leu	TCC Ser	CAC His	CCC Pro 345	CAC His	TTT Phe	TAC Tyr	AAC Asn 350	GCC Ala	GAC Asp	CCT Pro	GTG Val	TTG Leu 350	1112
TCA Ser 355	GAA Glu	GCT Ala	GTT Val	CTT Leu	GGT Gly 360	CTG Leu	AAC Asn	CCT Pro	AAC Asn	CCA Pro 365	AAG Lys	GAG Glu	CAT His	TCC Ser 370	TTG Leu 370	1160
TTC Phe	CTA Leu	GAC Asp	ATC Ile	CAT His 375	CCG Pro	GTC Val	ACT Thr	GGG Gly	ATC Ile 380	CCC Pro	ATG Met	AAC Asn	TGT Cys	TCT Ser 385	GTG Val 385	1208
AAG Lys	ATG Met	CAG Gln	CTG Leu	AGC Ser	CTC Leu	TAC Tyr	ATC Ile	AAA Lys	TCT Ser	GTC Val	AAG Lys	GGC Gly	ATC Ile	GGG Gly	CAA Gln 1256	1256

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390										395										400										
ACA	GGG	AAG	ATC	GAG	CCA	GTA	GTT	CTG	CCG	TTG	CTG	TGG	TTC	GAA	CAG		1304													
Thr	Gly	Lys	Ile	Glu	Pro	Val	Val	Leu	Pro	Leu	Leu	Trp	Phe	Glu	Gln															
		405					410					415																		
AGC	GGA	GCA	ATG	GGT	GGC	AAG	CCC	CTG	AGC	ACG	TTC	TAC	ACG	CAG	CTG		1352													
Ser	Gly	Ala	Met	Gly	Gly	Lys	Pro	Leu	Ser	Thr	Phe	Tyr	Thr	Gln	Leu															
		420				425					430																			
GTG	CTG	ATG	CCC	CAG	GTT	CTT	CAC	TAC	GCG	CAG	TAT	GTG	CTG	CTG	GGG		1400													
Val	Leu	Met	Pro	Gln	Val	Leu	His	Tyr	Ala	Gln	Tyr	Val	Leu	Leu	Gly															
		435				440				445					450															
CTT	GGA	GGC	CTC	CTG	TTG	CTG	GTG	CCC	ATC	ATC	TGC	CAA	CTG	CGC	AGC		1448													
Leu	Gly	Gly	Leu	Leu	Leu	Leu	Val	Pro	Ile	Ile	Cys	Gln	Leu	Arg	Ser															
				455					460					465																
CAG	GAG	AAA	TGC	TTT	TTG	TTT	TGG	AGT	GGT	AGT	AAA	AAG	GGC	TCC	CAG		1496													
Gln	Glu	Lys	Cys	Phe	Leu	Phe	Trp	Ser	Gly	Ser	Lys	Lys	Gly	Ser	Gln															
			470					475					480																	
GAT	AAG	GAG	GCC	ATT	CAG	GCC	TAC	TCT	GAG	TCC	CTG	ATG	TCA	CCA	GCT		1544													
Asp	Lys	Glu	Ala	Ile	Gln	Ala	Tyr	Ser	Glu	Ser	Leu	Met	Ser	Pro	Ala															
		485					490					495																		
GCC	AAG	GGC	ACG	GTG	CTG	CAA	GAA	GCC	AAG	CTA	TAGGGTCCTG	AAGACACTAT				1597														
Ala	Lys	Gly	Thr	Val	Leu	Gln	Glu	Ala	Lys	Leu																				
		500				505																								
AAGCCCCCA	AACCTGATAG	CTTGGTCAGA	CCAGCCACCC	AGTCCCTACA	CCCCGCTTCT											1657														
TGAGGACTCT	CTCAGCGGAC	AGCCCACCAG	TGCCATGGCC	TGAGCCCCCA	GATGTCACAC											1717														
CTGTCCGCAC	GCACGGCACA	TGGATGCCCA	CGCATGTGCA	AAAACAACCTC	AGGGACCAGG											1777														
GACAGACC																1785														

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc. feature
 (B) LOCATION: 1..509

(D) OTHER INFORMATION: /Function = "Amino acid sequence for the murine Scavenger Receptor Class BI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Gly	Gly	Ser	Ser	Arg	Ala	Arg	Trp	Val	Ala	Leu	Gly	Leu	Gly	Ala
1				5					10					15	
Leu	Gly	Leu	Leu	Phe	Ala	Ala	Leu	Gly	Val	Val	Met	Ile	Leu	Met	Val
		20						25					30		
Pro	Ser	Leu	Ile	Lys	Gln	Gln	Val	Leu	Lys	Asn	Val	Arg	Ile	Asp	Pro
		35					40					45			
Ser	Ser	Leu	Ser	Phe	Gly	Met	Trp	Lys	Glu	Ile	Pro	Val	Pro	Phe	Tyr
		50				55					60				
Leu	Ser	Val	Tyr	Phe	Phe	Glu	Val	Val	Asn	Pro	Asn	Glu	Val	Leu	Asn
		65			70				75					80	
Gly	Gln	Lys	Pro	Val	Val	Arg	Glu	Arg	Gly	Pro	Tyr	Val	Tyr	Arg	Glu
			85						90					95	
Phe	Arg	Gln	Lys	Val	Asn	Ile	Thr	Phe	Asn	Asp	Asn	Asp	Thr	Val	Ser

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100								105				110							
Phe	Val	Glu	Asn	Arg	Ser	Leu	His	Phe	Gln	Pro	Asp	Lys	Ser	His	Gly				
		115					120					125							
Ser	Glu	Ser	Asp	Tyr	Ile	Val	Leu	Pro	Asn	Ile	Leu	Val	Leu	Gly	Gly				
	130					135					140								
Ser	Ile	Leu	Met	Glu	Ser	Lys	Pro	Val	Ser	Leu	Lys	Leu	Met	Met	Thr				
	145				150					155					160				
Leu	Ala	Leu	Val	Thr	Met	Gly	Gln	Arg	Ala	Phe	Met	Asn	Arg	Thr	Val				
				165					170					175					
Gly	Glu	Ile	Leu	Trp	Gly	Tyr	Asp	Asp	Pro	Phe	Val	His	Phe	Leu	Asn				
			180						185				190						
Thr	Tyr	Leu	Pro	Asp	Met	Leu	Pro	Ile	Lys	Gly	Lys	Phe	Gly	Leu	Phe				
		195					200					205							
Val	Gly	Met	Asn	Asn	Ser	Asn	Ser	Gly	Val	Phe	Thr	Val	Phe	Thr	Gly				
	210					215					220								
Val	Gln	Asn	Phe	Ser	Arg	Ile	His	Leu	Val	Asp	Lys	Trp	Asn	Gly	Leu				
	225				230					235					240				
Ser	Lys	Ile	Asp	Tyr	Trp	His	Ser	Glu	Gln	Cys	Asn	Met	Ile	Asn	Gly				
				245					250					255					
Thr	Ser	Gly	Gln	Met	Trp	Ala	Pro	Phe	Met	Thr	Pro	Glu	Ser	Ser	Leu				
			260						265				270						
Glu	Phe	Phe	Ser	Pro	Glu	Ala	Cys	Arg	Ser	Met	Lys	Leu	Thr	Tyr	Asn				
		275					280					285							
Glu	Ser	Arg	Val	Phe	Glu	Gly	Ile	Pro	Thr	Tyr	Arg	Phe	Thr	Ala	Pro				
	290					295					300								
Asp	Thr	Leu	Phe	Ala	Asn	Gly	Ser	Val	Tyr	Pro	Pro	Asn	Glu	Gly	Phe				
	305				310					315					320				
Cys	Pro	Cys	Arg	Glu	Ser	Gly	Ile	Gln	Asn	Val	Ser	Thr	Cys	Arg	Phe				
				325					330					335					
Gly	Ala	Pro	Leu	Phe	Leu	Ser	His	Pro	His	Phe	Tyr	Asn	Ala	Asp	Pro				
			340						345				350						
Val	Leu	Ser	Glu	Ala	Val	Leu	Gly	Leu	Asn	Pro	Asn	Pro	Lys	Glu	His				
		355					360					365							
Ser	Leu	Phe	Leu	Asp	Ile	His	Pro	Val	Thr	Gly	Ile	Pro	Met	Asn	Cys				
	370					375					380								
Ser	Val	Lys	Met	Gln	Leu	Ser	Leu	Tyr	Ile	Lys	Ser	Val	Lys	Gly	Ile				
	385				390					395					400				
Gly	Gln	Thr	Gly	Lys	Ile	Glu	Pro	Val	Val	Leu	Pro	Leu	Leu	Trp	Phe				
				405					410					415					
Glu	Gln	Ser	Gly	Ala	Met	Gly	Gly	Lys	Pro	Leu	Ser	Thr	Phe	Tyr	Thr				
			420						425				430						
Gln	Leu	Val	Leu	Met	Pro	Gln	Val	Leu	His	Tyr	Ala	Gln	Tyr	Val	Leu				
		435					440					445							
Leu	Gly	Leu	Gly	Gly	Leu	Leu	Leu	Val	Pro	Ile	Ile	Cys	Gln	Leu					
	450					455				460									
Arg	Ser	Gln	Glu	Lys	Cys	Phe	Leu	Phe	Trp	Ser	Gly	Ser	Lys	Lys	Gly				
	465				470					475					480				

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Ser	Gln	Asp	Lys	Glu	Ala	Ile	Gln	Ala	Tyr	Ser	Glu	Ser	Leu	Met	Ser
				485					490					495	
Pro	Ala	Ala	Lys	Gly	Thr	Val	Leu	Gln	Glu	Ala	Lys	Leu			
			500					505							

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